

aattgtggct	gtggaactgt	caactggagg	tcctgcacat	gcaattcagg	gaaaaccgtg	60
aaaaagtatc	atgaggtatt	acagtttgag	cctggccaca	tcaagaggag	gggtagagct	120
aagaccatgg	ctctagttga	catccagttg	gatcaccatg	aacgatgtga	ttgtatctgc	180
agctcaagac	cacctcgata	agagaatgtg	cacatcctta	cattaagcct	gaaagaacca	240
ttagtttaag	gagggtgaga	taagagacc	ttttctacc	agcaaccga	cttactacta	300
gcctgcaatg	caatgaacac	aagtggttgc	tgaqtctcag	ccttgctttg	ttaatgccat	360

Fig. 1

```

Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
  1          5          10          15
Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
          20          25          30
His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
          35          40          45
Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
          50          55          60
Pro Arg
65

```

Fig. 2

ggaagatttc	caaccgcag	cagcttcaga	gaccaactgg	aatctgtcac	aagctctgtt	60
tcagggtatc	cctataactc	tccatcagta	acggatccca	ctctgattgc	ggatgctctg	120
gacaaaaaaa	ttgcagaatt	tgatacagtg	gaagatctgc	tcaagtaact	caatccagag	180
tcatggcaag	aagatcttta	gaatatgtat	ctggacaccc	ctcggtatcg	aggcaggtca	240
taccatgacc	ggaagtcгаа	agttgacctg	ataaggctca	atgatgatgc	caagcggtac	300
agttgcactc	ccaggaaatta	ctcggctcaat	ataagagaag	agctgaagtt	ggccaattgtg	360
gtcttctttc	cacgttgcct	cctcgtgcag	cgctgtggag	gaaattgttg	ctgtggaact	420
gtcaaactgg	agtctcgcac	atgcaattca	gggaaaaccg	tgaaaaagta	tcatgaggta	480
ttacagtttg	agcctggcca	catcaagagg	aggggtagag	ctaagaccat	ggctctagtt	540
gacatccagt	tggatcacca	tgaacgatgc	gattgtatct	gcagctcaag	accacctcga	600
taagagaatg	tgcacatcct	tacattaaag	ctgaaagaac	cttttagttta	aggaggggtga	660
gataagagac	ccttttccta	ccaqcaaccc				690

Fig. 3

Gly Arg Phe Pro Thr Arg Ser Ser Phe Arg Asp Gln Leu Glu Ser Val  
 1 5 10 15  
 Thr Ser Ser Val Ser Gly Tyr Pro Tyr Asn Ser Pro Ser Val Thr Asp  
 20 25 30  
 Pro Thr Leu Ile Ala Asp Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp  
 35 40 45  
 Thr Val Glu Asp Leu Leu Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu  
 50 55 60  
 Asp Leu Glu Asn Met Tyr Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser  
 65 70 75 80  
 Tyr His Asp Arg Lys Ser Lys Val Asp Leu Asp Arg Leu Asn Asp Asp  
 85 90 95  
 Ala Lys Arg Tyr Ser Cys Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg  
 100 105 110  
 Glu Glu Leu Lys Leu Ala Asn Val Val Phe Phe Pro Arg Cys Leu Leu  
 115 120 125  
 Val Gln Arg Cys Gly Gly Asn Cys Gly Cys Gly Thr Val Lys Leu Glu  
 130 135 140  
 Ser Cys Thr Cys Asn Ser Gly Lys Thr Val Lys Lys Tyr His Glu Val  
 145 150 155 160  
 Leu Gln Phe Glu Pro Gly His Ile Lys Arg Arg Gly Arg Ala Lys Thr  
 165 170 175  
 Met Ala Leu Val Asp Ile Gln Leu Asp His His Glu Arg Cys Asp Cys  
 180 185 190  
 Ile Cys Ser Ser Arg Pro Pro Arg  
 195 200

Fig. 4

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ttgtaccgaa gagatgagac catccaggtg aaaggaaacg gctacgtgca ggtcctaga 60
ttcccgaaca gctaccccag gaacctgctc ctgacatggc ggcttcactc tcaggagaat 120
acacggatac agctagtgtt tgacaatcag tttggattag aggaagcaga aaatgatatc 180
tgtaggtatg attttgtgga agttgaagat atatccgaaa ccagtaccat tattagagga 240
cgatgggtgtg gacacaagga agttcctcca aggataaaaat caagaacgaa ccaaattaaa 300
atcacattca agtccgatga ctactttgtg gctaaacctg gattcaagat ttattattct 360
ttgctggaag atttccaacc cgcagcagct tcagagacca actgggaatc tgtcacaagc 420
tctatttcag gggatatccta taactctcca tcagtaacgg atcccactct gattgcggat 480
gctctggaca aaaaaattgc agaatttgat acagtggag agtctgctcaa gtacttcaat 540
ccagagtcac ggcaagaaga tcttgagaat atgtatctgg acaccctcgg gtatcgaggc 600
aggtcatacc atgaccggaa gtcaaaaagt gacctggata ggctcaatga tgatgccaaag 660
cgttacagtt gcaactcccag gaattactcg gtcaatataa gagaagagct gaagttggcc 720
aatgtggtct tctttccacg ttgcctcctc gtgcagcgtc gtggaggaaa ttgtggctgt 780
ggaactgtca actggagggtc ctgcacatgc aattcaggga aaaccgtgaa aaagtatcat 840
gaggtattac agtttgagcc tggccacatc aagaggagggt gtagagctaa gaccatggct 900
ctagttgaca tccagttgga tcaccatgaa cgatgcgatt gtatctgcag ctcaagacca 960
cctcgataag agaattgtga catccttaca ttaagcctga aagaaccttt agtttaagga 1020
gggtgagata agagaccttt ttcctaccag caaccaaact tactactagc ctgcaatgca 1080
atgaacacaa gtggttgctg agtctcagcc ttgctttgtt aatgccatgg caagtagaaa 1140
ggtatatcat caacttctat acctaagaat ataggattgc atttaataat agtgtttgag 1200
ggtatatatg cacaaaacac cacagaaata tattcatgtc tatgtgtata tagatcaaat 1260
gttttttttg gtatatataa ccaggtacac cagagcttac atatgtttga gttagactct 1320
taaaatcctt tgccaaaata agggatgggtc aaatatatga aacatgtctt tagaaaattt 1380
aggagataaa tttattttttt aattttgaaa cacaaaacaa ttttgaatct tgctctctta 1440
aagaaagcat cttgtatatt aaaaatcaaa agatgagggt ttcttacata tacatcttag 1500
ttgattatta aaaaaggaaa aagggtttcca gagaaaaggc caatacctaa gcattttttc 1560
catgagaagc actgcatact tacctatgtg gactgtaata acctgtctcc aaaaccatgc 1620
cataataata taagtgtctt agaaattaaa tcattgtgtt ttttatgcat tttgctgagg 1680
catccttatt catttaacac ctatctcaaa aacttactta gaagggtttt tattatagtc 1740
ctacaaaaga caatgtataa gctgtaacag aattttgaat tgtttttctt tgcaaaaacc 1800
ctccacaaaa gcaaatcctt tcaagaatgg catgggcatt ctgtatgaac ctttccagat 1860
ggtgttcagt gaaagatgtg ggtagttgag aacttaaaaa gtgaacattg aaacatcgac 1920
gtaactggaa accg

```

Fig. 5

```

Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val
 1          5          10          15

Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
 20          25          30

Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
 35          40          45

Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
 50          55          60

Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
 65          70          75          80

Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
 85          90          95

```

Fig. 6

Fig. 6 cont.

Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys  
 100 105 110  
 Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala  
 115 120 125  
 Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly  
 130 135 140  
 Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp  
 145 150 155 160  
 Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu  
 165 170 175  
 Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr  
 180 185 190  
 Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser  
 195 200 205  
 Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys  
 210 215 220  
 Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala  
 225 230 235 240  
 Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly  
 245 250 255  
 Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser  
 260 265 270  
 Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly  
 275 280 285  
 His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile  
 290 295 300  
 Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro  
 305 310 315 320  
 Pro Arg

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cgctcggaaa gttcagcatg caggaagttt ggggagagct cggcgattag cacagcgacc	60
cgggccagcg cagggcgagc gcagggcgcg agagcgagg gcggcgcggc gtcggtccc	120
ggagcagaac ccggcttttt cttggagcga cgctgtctct agtcgctgat cccaa	175
atg cac cgg ctc atc ttt gtc tac act cta atc tgc gca aac ttt tgc	223
Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys	
1 5 10 15	
agc tgt cgg gac act tct gca acc ccg cag agc gca tcc atc aaa gct	271
Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala	
20 25 30	
ttg cgc aac gcc aac ctc agg cga gat gag agc aat cac ctc aca gac	319
Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp	
35 40 45	
ttg tac cga aga gat gag acc atc cag gtg aaa gga aac ggc tac gtg	367
Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val	
50 55 60	
cag agt cct aga ttc ccg aac agc tac ccc agg aac ctg ctc ctg aca	415
Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr	
65 70 75 80	
tgg cgg ctt cac tct cag gag aat aca cgg ata cag cta gtg ttt gac	463
Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp	
85 90 95	
aat cag ttt gga tta gag gaa gca gaa aat gat atc tgt agg tat gat	511
Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp	
100 105 110	
ttt gtg gaa gtt gaa gat ata tcc gaa acc agt acc att att aga gga	559
Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly	
115 120 125	
cga tgg tgt gga cac aag gaa gtt cct cca agg ata aaa tca aga acg	607
Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr	
130 135 140	
aac caa att aaa atc aca ttc aag tcc gat gac tac ttt gtg gct aaa	655
Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys	
145 150 155 160	

Fig. 7

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Fig. 7 cont.

cct gga ttc aag att tat tat tct ttg ctg gaa gat ttc caa ccc gca	703
Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala	
165 170 175	
gca gct tca gag acc aac tgg gaa tct gtc aca agc tct att tca ggg	751
Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly	
180 185 190	
gta tcc tat aac tct cca tca gta acg gat ccc act ctg att gcg gat	799
Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp	
195 200 205	
gct ctg gac aaa aaa att gca gaa ttt gat aca gtg gaa gat ctg ctc	847
Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu	
210 215 220	
aag tac ttc aat cca gag tca tgg caa gaa gat ctt gag aat atg tat	895
Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr	
225 230 235 240	
ctg gac acc cct cgg tat cga ggc agg tca tac cat gac cgg aag tca	943
Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser	
245 250 255	
aaa gtt gac ctg gat agg ctc aat gat gat gcc aag cgt tac agt tgc	991
Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys	
260 265 270	
act ccc agg aat tac tcg gtc aat ata aga gaa gag ctg aag ttg gcc	1039
Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala	
275 280 285	
aat gtg gtc ttc ttt cca cgt tgc ctc ctc gtg cag cgc tgt gga gga	1087
Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly	
290 295 300	
aat tgt ggc tgt gga act gtc aac tgg agg tcc tgc aca tgc aat tca	1135
Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser	
305 310 315 320	
ggg aaa acc gtg aaa aag tat cat gag gta tta cag ttt gag cct ggc	1183
Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly	
325 330 335	

Fig. 7 cont.

cac atc aag agg agg ggt aga gct aag acc atg gct cta gtt gac atc 1231  
 His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile  
 340 345 350

cag ttg gat cac cat gaa cga tgc gat tgt atc tgc agc tca aga cca 1279  
Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro  
355 360 365

cct cga taagagaatg tgcacatcct tacattaagc ctgaaagaac ctttagttta 1335  
Pro Arg  
370

aggagggtga	gataagagac	ccttttccta	ccagcaacca	aacttactac	tagcctgcaa	1395
tgcaatgaac	acaagtgggt	gctgagtctc	agccttgctt	tgtaaatgcc	atggcaagta	1455
gaaaggtata	tcatcaactt	ctatacctaa	gaatatagga	ttgcatttaa	taatagtgtt	1515
tgaggttata	tatgcacaaa	cacacacaga	aatatattca	tgtctatgtg	tatatagatc	1575
aaatgttttt	tttggttata	ataaaccggt	acacCagagc	ttacatatgt	ttgagttaga	1635
ctcttaaaat	cctttgccaa	aataagggat	ggtcaaatat	atgaaacatg	tctttagaaa	1695
atntagggaga	taaattttatt	tttaaatttt	gaaacacaaa	acaattttga	atcttgctct	1755
cttaaagaaa	gcatcttgta	tattaaaaat	caaaagatga	ggctttctta	catatacatc	1815
ttagttgatt	attaaaaaag	gaaaaagggt	tccagagaaa	aggccaatac	ctaagcattt	1875
tttccatgat	aagcactgca	tacttaccta	tgtggactgt	aataaacctgt	ctccaaaacc	1935
atgccataat	aatataagtg	ccttagaaat	taaatcattg	tgttttttat	gcattttgct	1995
gaggcatcct	tattcattta	acacctatct	caaaaactta	cttagaaggt	tttttattat	2055
agtcctacaa	aagacaatgt	ataagctgta	acagaatttt	gaattgtttt	tctttgcaaa	2115
acccctccac	aaaagcaaat	cctttcaaga	atggcatggg	cattctgtat	gaacctttcc	2175
agatggtgtg	cagtgaaga	tgtgggtagt	tgagaactta	aaaagtgaac	attgaaacat	2235
cgacgtaact	ggaaaccg					2253

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Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe  
1 5 10 15

Cys Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys  
20 25 30

Ala Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr  
35 40 45

Asp Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr  
50 55 60

Val Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu  
65 70 75

Thr Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe  
80 85 90 95

Asp Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr  
100 105 110

Asp Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg  
115 120 125

Gly Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg  
130 135 140

Thr Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala  
145 150 155

Lys Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro  
160 165 170 175

Ala Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser  
180 185 190

Gly Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala  
195 200 205

Asp Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu  
210 215 220

Leu Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met  
225 230 235

Fig. 8

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Fig. 8 cont.

Tyr Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys  
240 245 250 255

Ser Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser  
260 265 270

Cys Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu  
275 280 285

Ala Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly  
290 295 300

Gly Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn  
305 310 315

Ser Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro  
320 325 330 335

Gly His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp  
340 345 350

Ile Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg  
355 360 365

Pro Pro Arg  
370

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PDGF-D M H R L I F V Y T L I G A N F C S C R O T S A T P Q S A S I K A L R N A N L R R 40  
 PDGF-C M S L F G L L L V T S A L A G Q R R G T Q A - - - - - E S N L S S K F Q F S S 34

PDGF-D D - E S N H L L T D L Y R R D E T I Q V K G N G Y V Q S P R F P N S Y P R N L L L 79  
 PDGF-C N K E Q N G V Q D P Q H E R I T - V S T N G S I H S P R F P H T Y P R N T V L 73

PDGF-D T W R L - H S O E N T R I Q L V F O N O F G L E E A E N D I C R Y O F V E V E D 118  
 PDGF-C V W R L V A V E E N V W I O L L T E D E R F G L E D P E D D I C K Y O F V E V E E 113

PDGF-D I S E T S T I I R G R W C G H K E V P P R I K S R T N Q I K I T F K S D O Y F V 158  
 PDGF-C P S D - - G T I I G R W C G S G T V P G K Q I S K G N Q T R I R F V S D E Y F P 151

PDGF-D A K P G F K I Y Y S L L E D F O P A A S E T N W E S V T S S I S G V S Y N S P 198  
 PDGF-C S E P G F C I H Y N I V M P Q F T E A V - - - - - - - - - - - S P 173

PDGF-D S V T D P - T L I A D A L D K K I A E F D T V E D L L K Y F N P E S W Q E O L E 237  
 PDGF-C S V L P D S A L P L D L L N A I T A F S T L E D L I R Y L E P E R W Q L D L E 213

PDGF-D N M Y L D T P R Y R G R S Y H D - R K S K V O L D R L N - D D A K R Y S C T P R 275  
 PDGF-C D L Y R P T W Q L L G K A F V F G R K S R V V D L N L L T E E V R L Y S C T P R 253

PDGF-D N Y S V N I R E E L K L A N V V F F P R C L L V Q R C G G N C G C G T V N W R S 315  
 PDGF-C N F S V S I R E E L K R T O T I E W P G C L L V K R C G G N C A C C L H N C N E 293

PDGF-D C T C N S G K T V K K Y H E V L Q F E P G H I K R R G R A K T M A L V D I O L D 355  
 PDGF-C C Q C V P S K V T K K Y H E V L Q L R P - K T G V R G - - L H K S L T D V A L E 330

PDGF-D H H E R C D C I C S S R P P R 370  
 PDGF-C H H E F C D C V C R G S T G G 345

Fig. 9

POGF-0	C	T	P	R	N	Y	S	V	N	I	-	R	E	E	L	K	L	A	N	V	V	F	-	F	P	R	C	L	L	V	Q	R	C	G	G	N	C	G	C	308
POGF-C	C	T	P	R	N	F	S	V	S	I	-	R	E	E	L	K	R	T	D	T	I	F	-	W	P	C	L	L	V	K	R	C	G	G	N	C	A	C	123	
POGF-A	C	K	T	R	T	V	I	Y	E	I	-	R	S	Q	V	O	P	T	S	A	N	F	L	I	W	P	C	V	E	V	K	R	C	G	G	-	C	132		
POGF-B	C	K	T	R	T	T	E	V	F	E	I	-	R	R	L	I	D	R	T	N	A	F	L	V	W	P	C	V	E	V	Q	R	C	G	G	-	C	133		
VEGF 165	C	H	P	I	E	T	L	V	O	I	-	Q	E	Y	P	S	E	E	I	E	Y	H	F	-	K	P	C	V	P	L	M	R	C	G	G	-	C	86		
PLGF-2	C	R	A	L	E	R	L	V	O	V	-	S	E	Y	P	S	E	V	E	H	M	F	-	S	P	C	V	S	L	L	L	R	C	G	G	-	C	86		
VEGF-82167	C	Q	P	R	E	V	V	P	L	T	-	V	E	L	M	G	T	V	A	K	Q	L	-	V	P	C	V	T	V	O	R	C	G	G	-	C	81			
VEGF-C	C	M	P	R	E	V	C	I	O	V	A	-	E	F	G	V	A	T	M	T	F	F	-	K	P	C	V	S	V	Y	R	C	G	G	-	C	165			
VEGF-D	C	S	P	R	E	T	C	V	E	V	A	-	E	L	G	K	T	T	N	T	F	F	-	K	P	C	V	N	V	F	R	C	G	G	-	C	150			

P0GF-0	G T V N W R S C T C N S G K T V K K Y H E V L Q F E P G H I K R R G R A K T M A	348
P0GF-C	C L H N C N E C Q C V P - S K V I T K K Y H E V L Q L R P K T G V R G L H K - - S	160
P0GF-A	C N T S S V K C Q P S R V H H R S V K V A K V E Y V R K K P K L - - - K E	166
P0GF-B	C N N R N V Q C R P T Q V Q L R P V Q V R K I E I V R K K P I F - - - K K	167
VEGF 165	C N O E G L E C V P T E S N I T M Q I M R I K - - - P H Q G Q - - - H I	117
PLGF-2	C G D E D L H C V P V E T A N Y I T M Q L L K I R - - - S G O R P - - - S Y	117
VEGF-R167	C P O O G L E C V P T G Q H Q V R M Q I L M I R Y - - P S S Q L - - - -	111
VEGF-C	C N S E G L Q C M N T S T S Y L S K T L F E I T V - - P L S Q G - - - P K	197
VEGF-D	C N E E G V M C M N T S T S Y I S K Q L F E I S V - - P L T S V - - - P E	182

POGF-D	L	V	D	I	Q	L	D	H	E	R	C	D	C
POGF-C	L	T	D	V	A	L	E	H	E	E	-	C	C
POGF-A	Y	Q	V	R	L	E	E	H	L	A	-	C	K
POGF-B	A	T	V	T	L	E	D	H	L	A	-	C	K
VEGF 165	G	E	M	S	F	L	Q	H	N	K	-	C	E
PIGF-2	V	E	L	T	F	S	Q	H	V	R	-	C	E
VEGF-B167	G	E	M	S	L	E	E	H	S	Q	-	C	E
VEGF-C	P	V	T	I	S	F	A	N	H	T	S	C	R
VEGF-D	L	V	P	V	K	I	A	N	H	T	S	C	R

**Fig. 10**

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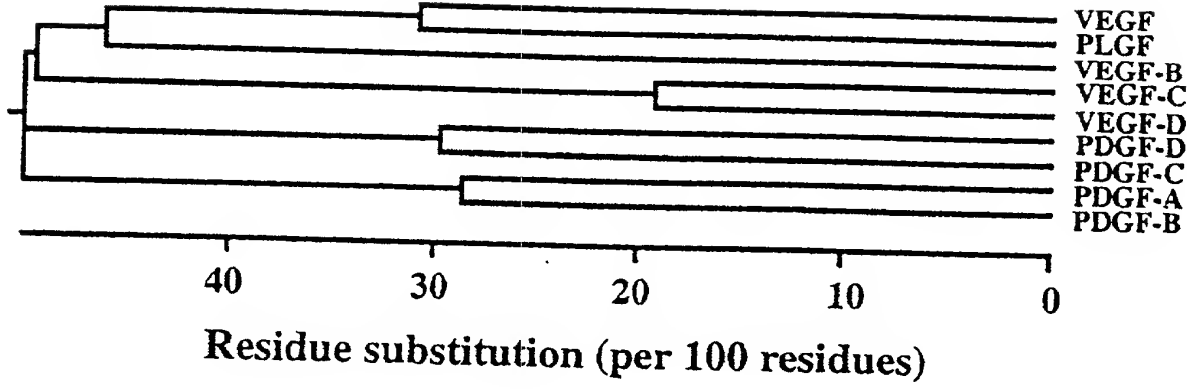


Fig. 11

R	NR
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 $M_r \times 10^{-3}$

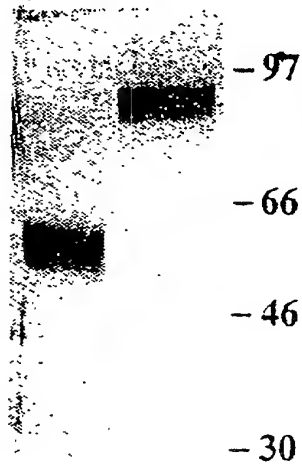


Fig. 13

hPDCF-D CUB	D E T I Q V K C N C Y V Q S P R F P N S Y P R N I L I T W R I L H S Q Q N T R I Q	I Q
hEMP-1 CUB1	C G E T Q Q C S T C N F S S P F E Y P M G Y S A H M H C I W R I S V T P G E F - K V	- K V
hEMP-1 CUB2	C G G D V Y K K D Y C H I Q S P F N Y P D D Y R P S K K V C I W R I O V S T P G C F - H V	- H V
hEMP-1 CUB3	C C C F I T K I E S P C V I T S P G W F K E Y P P K K N C I W Q I V A P T Q Y - R I	- R I
Neuropilin CUB1	C D T I K I E S P C V I T S P G W F K E Y P P K K N C I W Q I V A P T Q Y - R I	- R I
Neuropilin CUB2	C S Q N Y T P S C V I T S P G W F K E Y P P K K N C I W Q I V A P T Q Y - R I	- R I
hPDCF-D CUB	L V F D N Q F G L E A - - - - - E N D I C R Y D F E V E D I S E T S T I I R	I R
hEMP-1 CUB1	I L M F T S - I D L Y R S R - - - - - L C W Y D Y Y E V R D G G W R K A P L D	P L D
hEMP-1 CUB2	G L T F C S - F E I E R H D - - - - - S C A Y D Y Y E V R D G G H S E S T L I I	I I
hEMP-1 CUB3	S I O F D F - F F T E G N D - - - - - V C K Y D - V E V P S G L T A D S K F E	E
Neuropilin CUB1	M - N F M P H F D L E D R D - - - - - C X Y D Y Y E V F D G E N E N G H F E	E
Neuropilin CUB2	I L E F E S - F D L E P D S N P P G C M F C R Y D R L E I W D G E P D V G C P H I	H I
hPDCF-D CUB	G R W C C H K E V P P B I K S R T N O I K I T P K S D D Y F V A K P G F F A V V Y	Y Y
hEMP-1 CUB1	G R F C C S - K L P P P I V S T D S R L W Y F F R S S G N W T Y F V A K P G F F A V V Y	Y Y
hEMP-1 CUB2	G E Y C C Y - E K P D I K S T S S R I L K P V S D G S I N K A - G F F A V N F	F
hEMP-1 CUB3	G K F C C S - E Z P P V T S Q Y N N M R L F F F S D N T V S K A - G F F A V N F	F
Neuropilin CUB1	G K F C C K - I A P P P V V S S G P P L F I K F F S D N T V S K A - G F F A V N F	F
Neuropilin CUB2	C E Y C C Q - K T T D G R - R S S G I L S M V F Y T D G A T A E - G F F A V N F	F
hPDCF-D CUB	S L I	I
hEMP-1 CUB1	E A I	I
hEMP-1 CUB2	F K	K
hEMP-1 CUB3	F S E	E
Neuropilin CUB1	E I	I
Neuropilin CUB2	S V I	I

Fig. 12

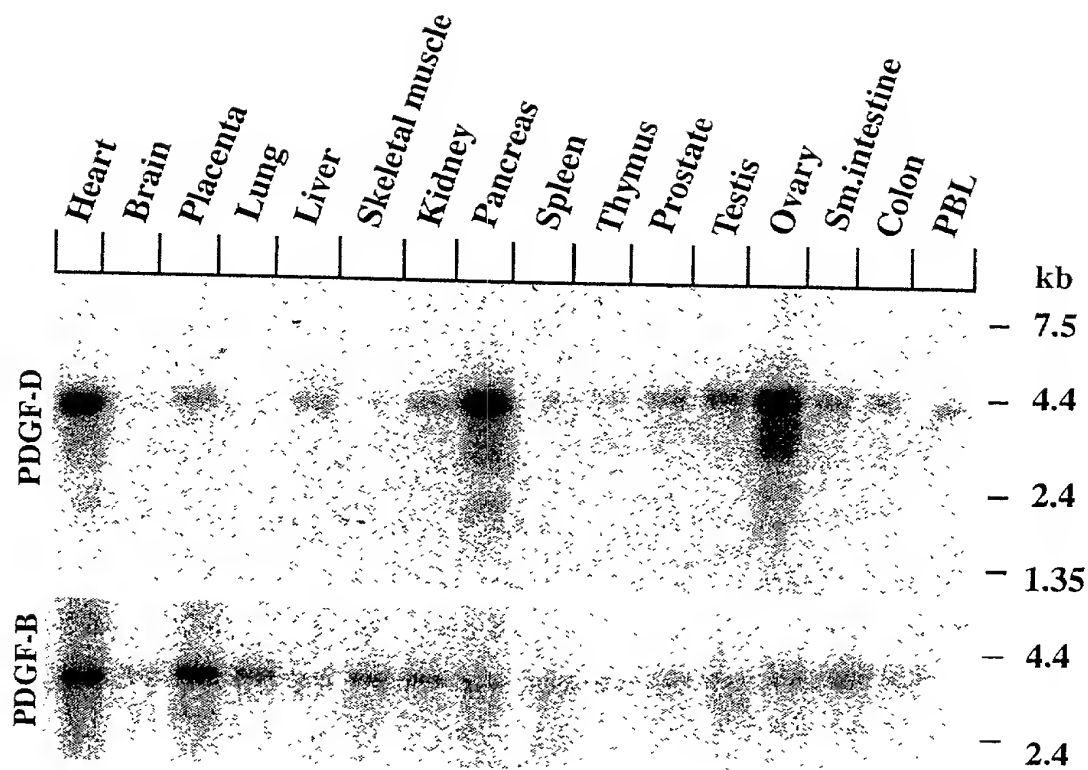


Fig. 14

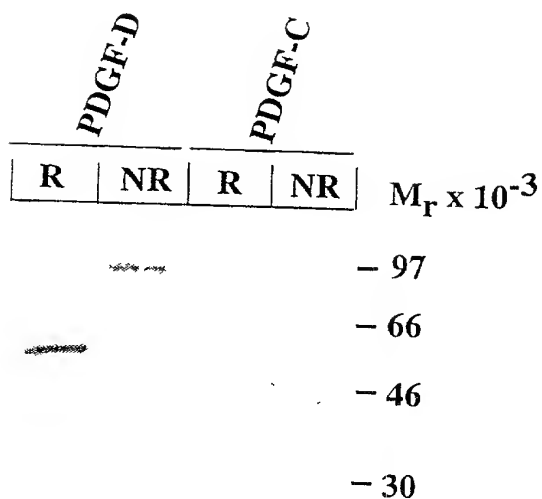


Fig. 15

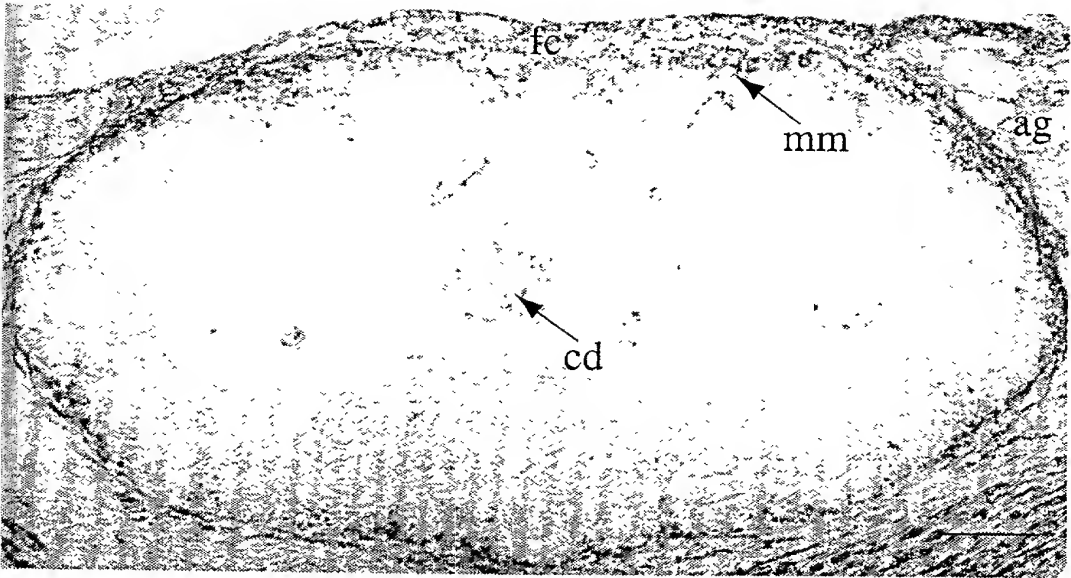


Fig. 16

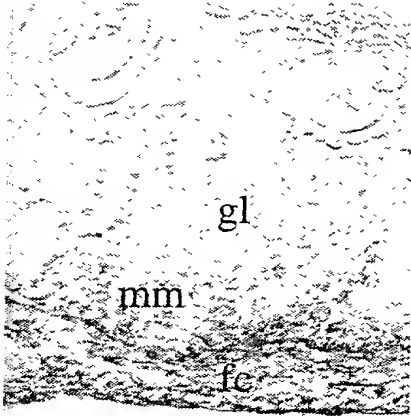


Fig. 17

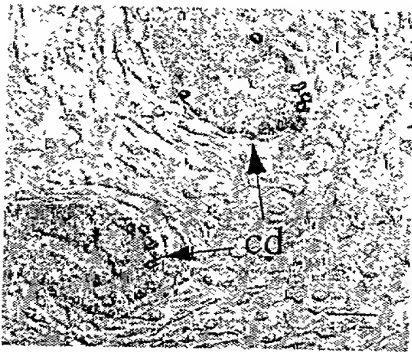


Fig. 18

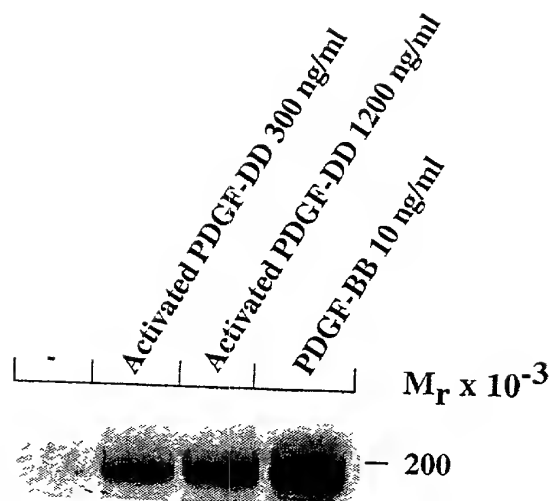


Fig. 19

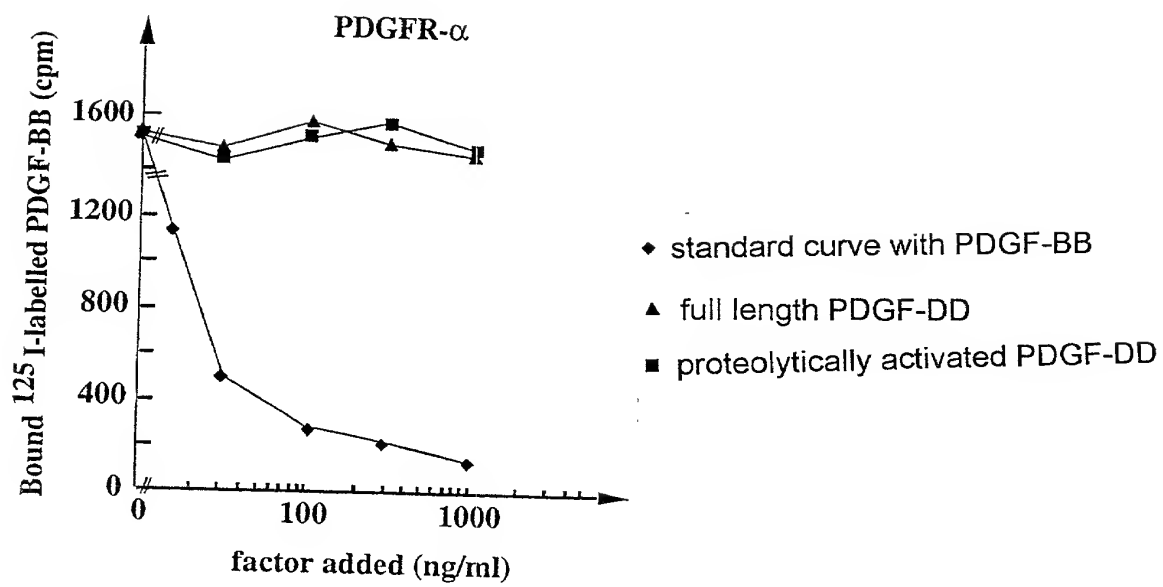


Fig. 20

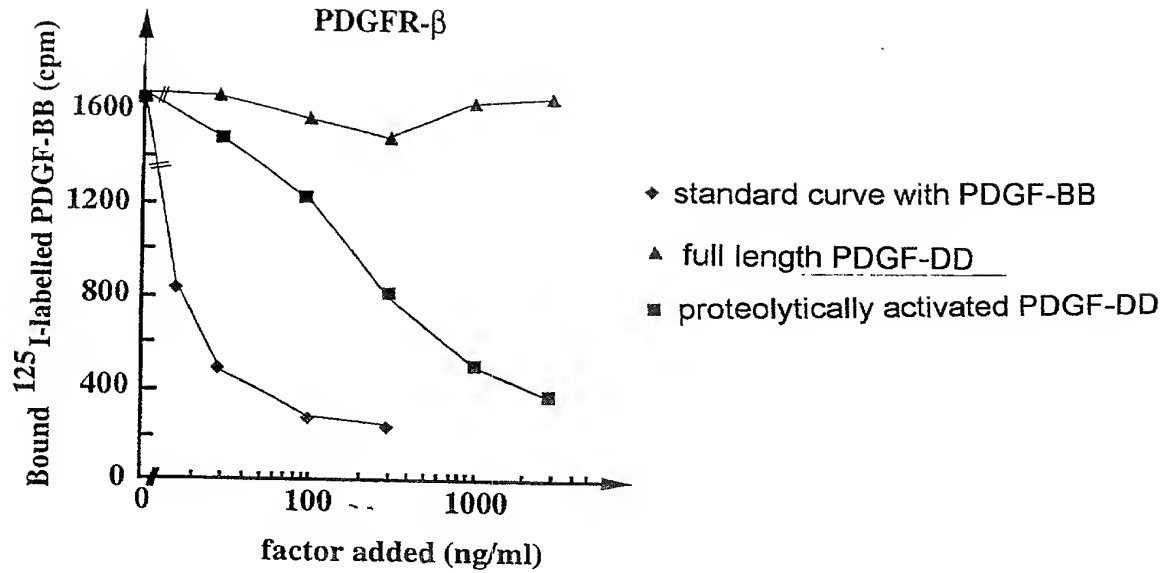


Fig. 21



Fig. 22A

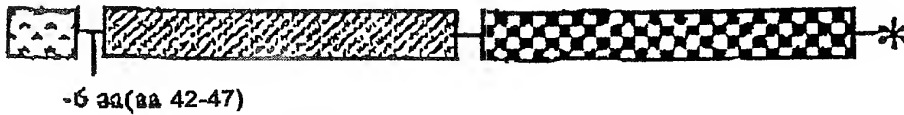


Fig. 22B

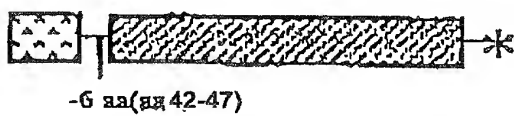
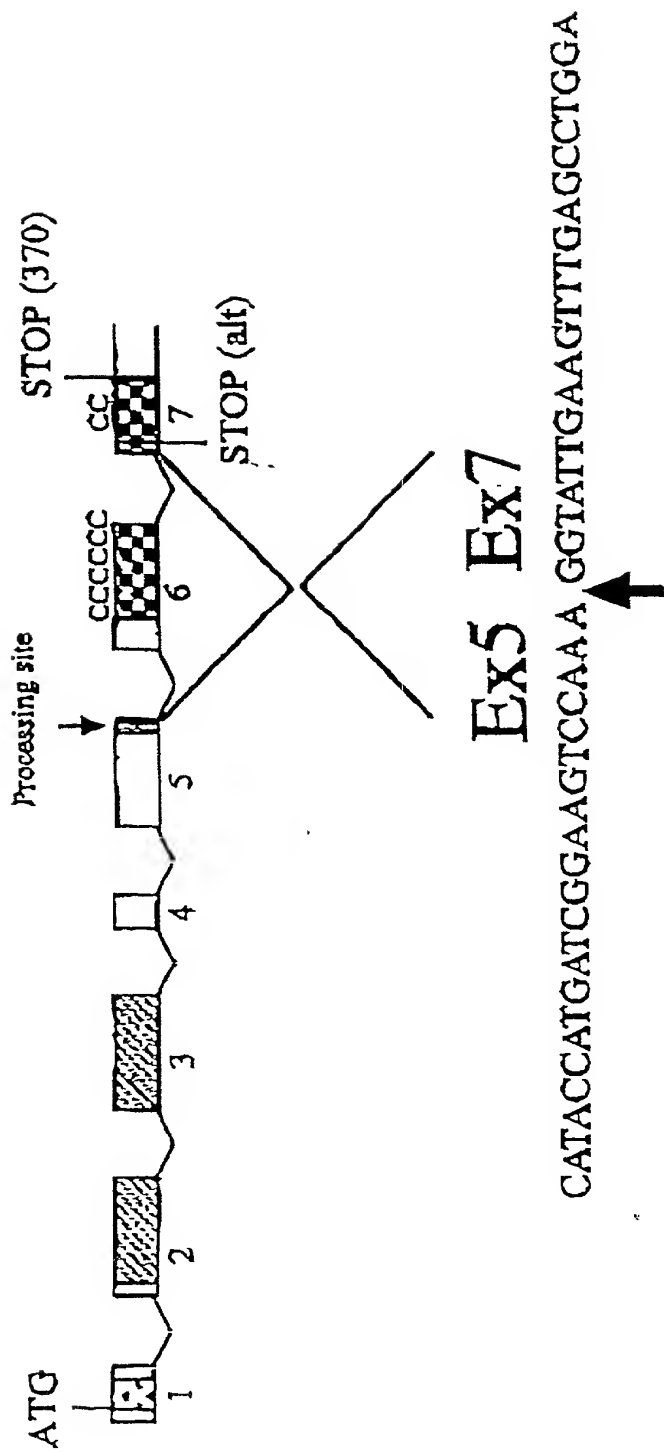


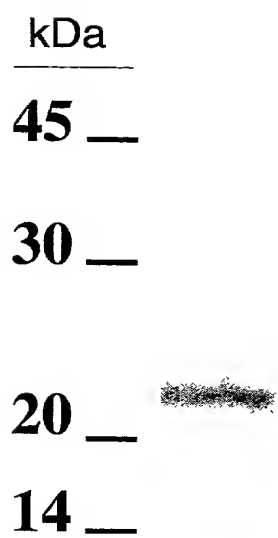
Fig. 22C

- Signal Sequence
- CUB
- PDGF



Signal Sequence  
CUB  
PDGF

Fig. 23



**Fig. 24**

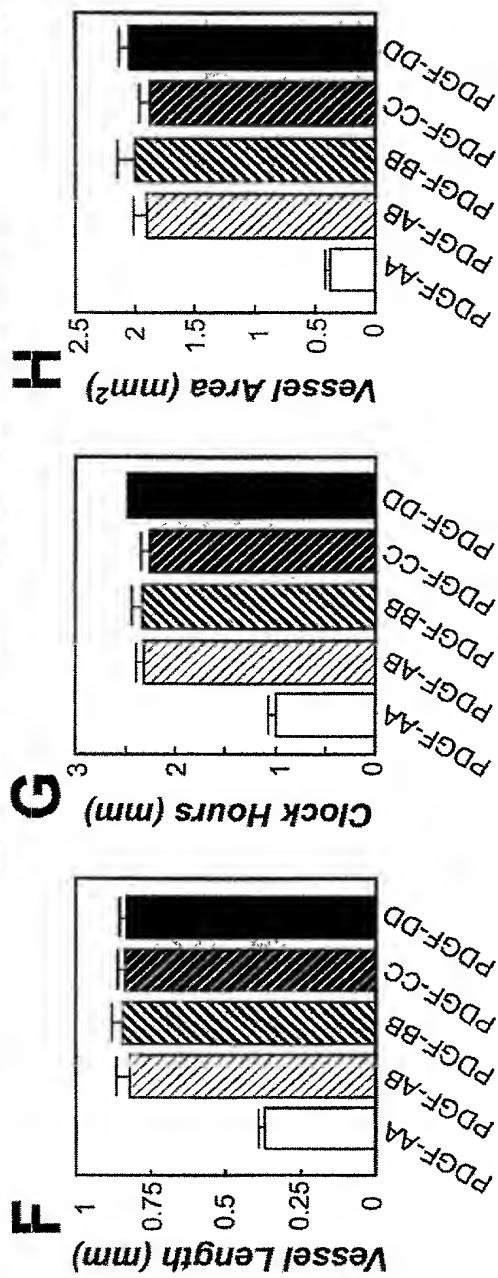
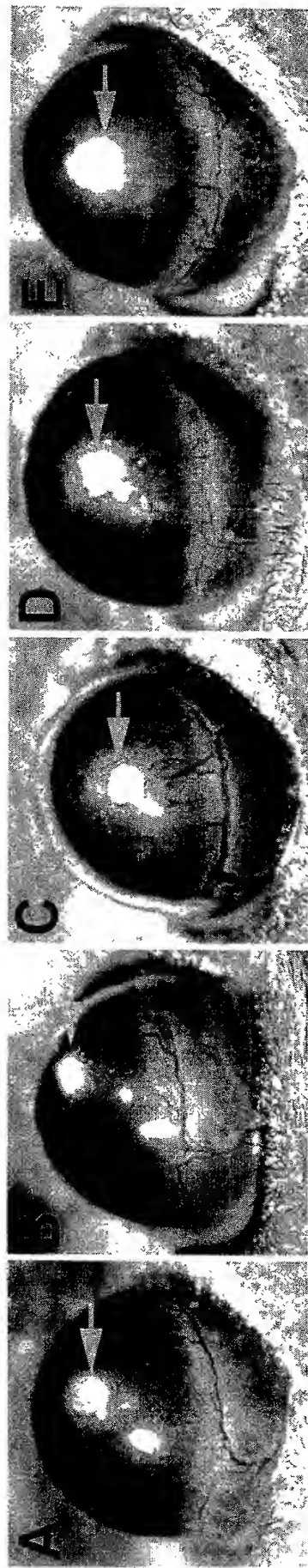


Fig. 25